

1/5

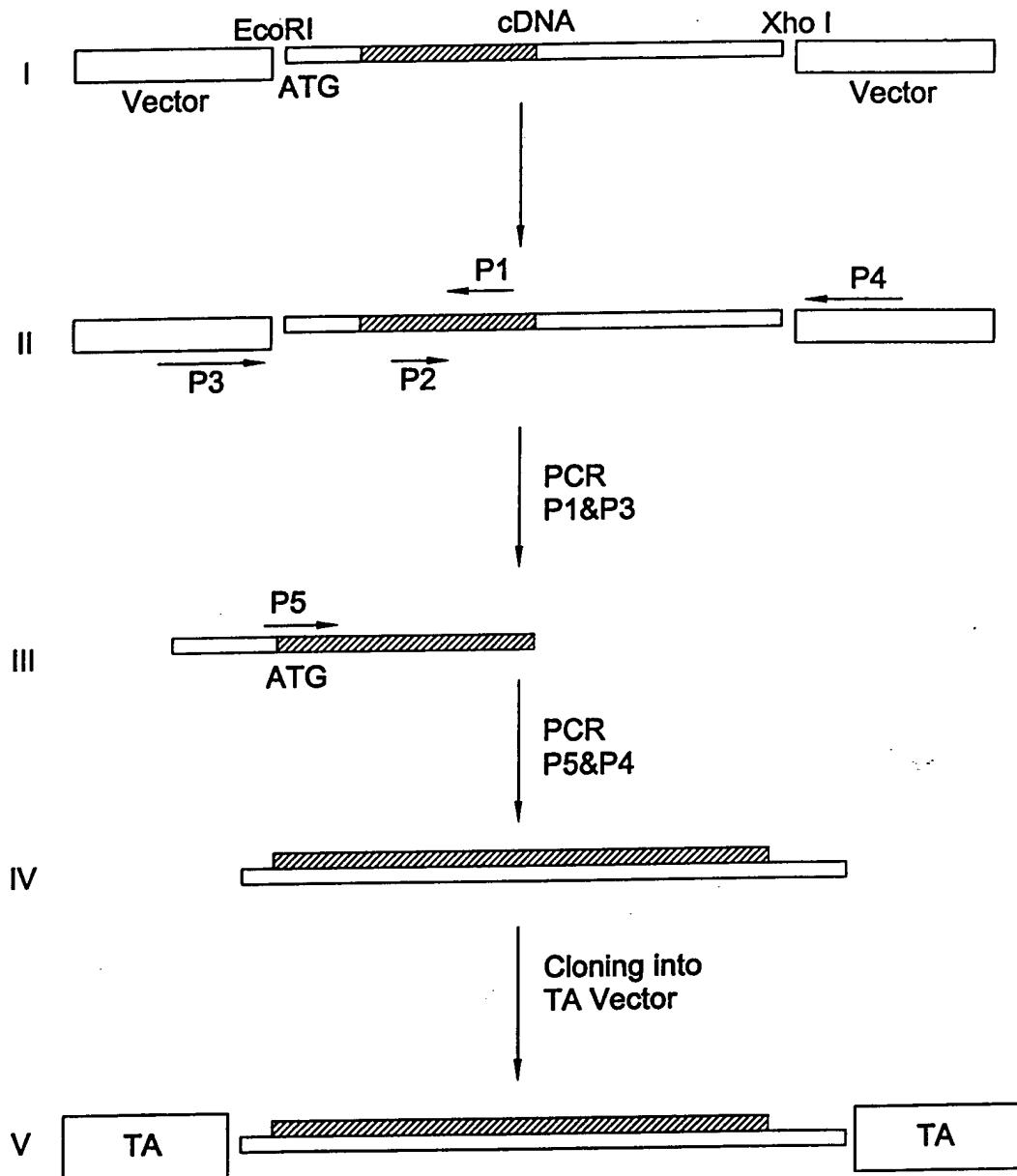


FIG. 1.

CLUSTAL W (1.7) multiple sequence alignment

FIG. 2.

CLUSTAL W (1.7) multiple sequence alignment

FIG. 3A.

4/5

P30986	PRLGYVNHIIDLGLGGIDWGNKTVVNNAI	EISRSWGESYF-LSNYERLIRAKTLIDPNNF
P93479	PRVGVVNHIIDLIGGIDWRNKSSTTNAVE	IARNWGERYF-SSNYERLKVAKTLIDPNNF
Sunf-19	PRAEFLNYRDL DIG-INSHGR	---NAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFF
Sunf-15	PRKAFLNYRDL DIG-INSHGR	---NAYTEGMVYGHKYFKETNYKRLVSVKTKVDPDNFF
BBE	PREAYMNYNDLDL G--FDS	---AAAYEEASEWGERYWKRENFKKLIRIKA KVDPENFF

P30986	NHPQSIPPMANFD--YLEKTLGSDGGEVV
P93479	NGPQSIPPMKFEIYMLKEL-----
Sunf-19	RNEQSIPTLSS-----
Sunf-15	RNEQSIPTLSS-----
BBE	RHPQSIPVFSRPLSDM-----

FIG. 3B.

5/5

CLUSTAL W (1.7) multiple sequence alignment

P30230	MAKFASIIIVLLFVALVVFAAFEEPTMVEAQKLCQRPSGTWSGVCGNNNACKNQCIRLEKA
P30231	-----QKLCEPSSGTWSGVCGNNNACKNQCINLEKA
P30224	MAKSATIVTLFFAALVFFAALEAPMVVEAQKLCERPSGTWSGVCGNSACKNQCINLEKA
defensin	MAKISVAFNAFLLLLFLVLAISEIGSVKG--ELCEKASQTWSGTCGKTHCDDQCKSWEWA
Q01784	MEKKSLAALSFLLLLVLFVAQEIVVTEA--NTCEHLADTYRGVCFTNASCDDHCKNKAHL

: *!! : *! *.* .. *,:;*

P30230	RHGSCNYVFPKAHKCICYFPC-----
P30231	RHGSCNYVFPKAHKCICYFPC-----
P30224	RHGSCNYVFPKAHKCICYFPC-----
defensin	AHGACHVRDGKHMCFCYFNCSAQKLAQDKLRAEELAKEKIEPEKATAKP
Q01784	ISGTCHD---WKCFCTQNC-----

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FIG. 4.